

## 7969076999.txt

## SEQUENCE LISTING

<110> Jackson, W. James  
 Pace, John  
 <120> Chlamydia Protein, Gene Sequence and Uses Thereof  
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 <140> 09/542,520  
 <141> 2000-04-03  
 <150> 08/942,596  
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 acgtgggttca tcgggtttcat aggctcgcca aatgggatat aggtggaaag gtaaaaaaaaa 180  
 ctgagccaag caaaggatag agaagtcctg taatcatcgc aggttaaaagg ggggatgtta 240  
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 aagataaagaa catttatttga tattaaattttaaattttttt atgaagcgga gtaattaaattt 360  
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 Ser Met Ile Leu Ala Tyr Ser Cys Cys Ser Leu Asn Gly Gly Tyr  
 15 20 25  
 gca gca gaa atc atg gtt cct caa gga att tac gat ggg gag acg tta 507  
 Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu  
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 act gta tca ttt ccc tat act gtt ata gga gat ccg agt ggg act act 555  
 Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr  
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 75 80 85 90  
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Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr		
140 145 150		
aca aca tct aca ccg tct aat ggt act att tat tct aaa aca gat ctt		891
Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu		
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Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly		
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Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly		
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Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu		
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 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
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 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
 65 70 75 80  
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
 85 90 95  
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 100 105 110  
 Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu  
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 130 135 140  
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 145 150 155 160  
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 195 200 205  
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
 210 215 220  
 Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn  
 225 230 235 240  
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 Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys  
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 Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser Ser  
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 370 375 380  
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785				790					795						800
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<220>  
 <221> modified\_base

## 7969076999.txt

<222> 12, 15		
<223> n = a, t, g, or c		
<400> 6		
gagagthatgg tnccncaa	18	
<210> 7		
<211> 18		
<212> DNA		
<213> Chlamydia sp.		
<220>		
<221> modified_base		
<222> 12, 15		
<223> n = a, t, g, or c		
<400> 7		
gagagthatgg tnccnccag	18	
<210> 8		
<211> 15		
<212> DNA		
<213> Chlamydia sp.		
<220>		
<221> modified_base		
<222> 1, 7		
<223> n = a, t, g, or c		
<400> 8		
ngtytcnccr tcata	15	
<210> 9		
<211> 15		
<212> DNA		
<213> Chlamydia sp.		
<220>		
<221> modified_base		
<222> 1, 7		
<223> n = a, t, g, or c		
<400> 9		
ngtytcnccr tcgta	15	
<210> 10		
<211> 1511		
<212> DNA		
<213> Chlamydia sp.		
<400> 10		
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actgttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaaaa	120	
aatcttgaca attctatigc agcttgcct ttaagtgtt ttggaaactt attaggagtt	180	
tttactgttt tagggagagg acactcgttg actttcgaga acatacggac ttctacaaat	240	
ggggcagctc taagtaatag cgctgtgtat ggactgtttt ctattgaggg tttaaagaa	300	
ttatccctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag	360	
ggtagccaga ctccgacgac aacatctaca ccgtctaatt gtactattta ttctaaaaca	420	
gatcttttgt tactcaataa tgagaagttc tcattctata gtaatttagt ctctggagat	480	
gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc	540	
caagaaaata ctgctcaagc tgatggggta gcttgtcaag tagicaccag ttctctgtct	600	
atggcttaacg aggctcctat tgccttgtt gctaatgtt caggagtaag agggggaggg	660	
attgctgctg ttcaaggatgg gcagcaggga gtgtcatcat ctacttcaac agaagatcca	720	

## 7969076999.txt

gtagtaagtt	tttccagaaa	tactgcggta	gagtttgatg	ggaacgtac	ccgagtagga	780
ggagggattt	actcctacgg	gaacgttgct	ttcctgaata	atggaaaaac	cttgtttctc	840
aacaatgtt	cttctccctgt	ttacattgtc	gctaagcaac	caacaagtgg	acaggcttc	900
aatacgaga	ataattacgg	agatggagga	gctatcttct	gtaagaatgg	tgcgcaagca	960
ggatccaata	actctggatc	atgttcctt	gatggagagg	gagtagttt	cttttagtagc	1020
aathtagctg	ctgggaaagg	gggagctatt	tatgccaataa	agctctcggt	tgctaactgt	1080
ggccctgtac	aatttttaag	gaatatacg	aatgatggtg	gagcgattta	tttaggagaa	1140
tctggagagc	tcagtttatac	tgctgattat	ggagatatta	ttttcgatgg	gaatcttaaa	1200
agaacagcca	aagagaatgc	tgccgatgtt	aatggcgtaa	ctgtgtcctc	acaagccatt	1260
tcgatggat	cgggagggaa	aataacgaca	ttaagagcta	aagcaggca	tcagattctc	1320
ttaatgatc	ccatcgagat	ggcaaacgga	aataaccagc	cagcgcagtc	ttccaaactt	1380
ctaaaaat	acgatggta	aggatcacaa	ggggatattt	tttttgctaa	tgaaagcagt	1440
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ttatcgtga	a					1511

<210> 11  
<211> 1444  
<212> DNA  
<213> Chlamydia sp.

<400> 11

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gcatttgcct	ctttcttctt	tgtttagcaa	caatgcagg	acgaatccctc	ctaccaatcc	180
tccagcgc	gattctcatac	ctgcagtc	ttgttagcaca	actgcgggtt	ctgttacaat	240
tagttggcct	atctttttt	aggattttga	tgatatacg	tatgataggt	atgattggct	300
aggttctaat	caaaaaatca	atgtcctgaa	attacagttt	gggactaagg	ccccagctaa	360
tgccccatca	gatttgactc	tagggatga	gatgcctaag	tatggctatc	aaggaagctg	420
gaagcttgcg	tgggatccca	atacagcaa	taatggctt	tatactctga	aagctacatg	480
gactaaaaact	gggtataatc	ctgggcctga	gchgagtagct	tctttggttc	caaatagttt	540
atgggatcc	attttagata	tacgatctgc	gcatttcagca	attcaagcaa	gtgtggatgg	600
gcgcctttat	tgtcgaggat	tatgggtttc	tggagtttcg	aattttttct	atcatgaccg	660
cgatgtttt	ggtcaggat	atcggtat	tagtgggggtt	tattctttag	gagcaaactc	720
ctacitttgg	tcatcgatgt	ttggtctagc	atttaccgaa	gtatttggta	gatctaaaga	780
ttatgtatgt	tgtcgatcca	atcatcatgc	ttgcatacgga	tccgtttatc	tatctacc	840
acaagcttta	tgtggatct	atttgttcgg	agatgcgtt	atccgtgc	gctacgggtt	900
tgggaatcc	catatgaaaa	cctcatatac	atttgcagag	gagagcgatg	ttcgttggga	960
taataactgt	ctggctggag	agattggagc	gggatttacc	attgtgat	ctccatctaa	1020
gctctattt	aatgagttgc	gtccttcgt	gcaagcttag	ttttctttag	ccgatcatga	1080
atcttttaca	gaggaaaggcg	atcaagctcg	ggcattcaag	agcggacatc	tcctaaatct	1140
atcagttcc	gttggagtga	agtttgatcg	atgttctagt	acacatcc	ataaataatag	1200
ctttatggcg	gcttatatact	gtgatctta	tcgcaccatc	tctggtactg	agacaacgct	1260
cctatccat	caagagacat	ggacaacaga	tgcccttcat	ttagcaagac	atggagttgt	1320
ggttagagga	tctatgtatg	tttctctaac	aagtaatata	gaagtatatg	gccatggaaag	1380
atatgagtt	cgagatgtt	ctcgaggctt	tgggttgagt	gcaggaagta	gagtccgggtt	1440
ctaa						1444

<210> 12  
<211> 56  
<212> DNA  
<213> Chlamydia sp.

<400> 12

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<210> 13  
<211> 56  
<212> DNA  
<213> Chlamydia sp.

<400> 13

aaggccccaa	ttacgcagag	ggtaccctaa	gaagaaggca	tgccgtgcta	gcggag	56
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## 7969076999.txt

<210> 14  
 <211> 57  
 <212> DNA  
 <213> Chlamydia sp.

<400> 14  
 aagggcccaa ttacgcagag ggtaccggag agctcgcgaa tccatacgaa taggaac 57

<210> 15  
 <211> 1013  
 <212> PRT  
 <213> Chlamydia sp.

<400> 15  
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr  
 1 5 10 15  
 Ser Cys Cys Ser Leu Asn Gly Gly Tyr Ala Ala Glu Ile Met Val  
 20 25 30  
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr  
 35 40 45  
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
 50 55 60  
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
 65 70 75 80  
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
 85 90 95  
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu  
 100 105 110  
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu  
 115 120 125  
 Leu Ser Phe Ser Asn Cys Asn Pro Leu Leu Ala Val Leu Pro Ala Ala  
 130 135 140  
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Ser Thr Thr Ser Thr Pro Ser  
 145 150 155 160  
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu  
 165 170 175  
 Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile  
 180 185 190  
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe  
 195 200 205  
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
 210 215 220  
 Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn  
 225 230 235 240  
 Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln  
 245 250 255  
 Gln Gly Val Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe  
 260 265 270  
 Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly  
 275 280 285  
 Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys  
 290 295 300  
 Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu  
 305 310 315 320  
 Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp  
 325 330 335  
 Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn  
 340 345 350  
 Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser  
 355 360 365  
 Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys Leu  
 370 375 380

## 7969076999.txt

ser Val Ala Asn Cys Gly Pro Val Gln Leu Leu Gly Asn Ile Ala Asn  
 385 390 395 400  
 Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser  
 405 410 415  
 Ala Asp Tyr Gly Asp Met Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala  
 420 425 430  
 Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala  
 435 440 445  
 Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala  
 450 455 460  
 Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn  
 465 470 475 480  
 Asn Gln Pro Ala Gln Ser Ser Glu Pro Leu Lys Ile Asn Asp Gly Glu  
 485 490 495  
 Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Asn Ser Thr Leu Tyr  
 500 505 510  
 Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala  
 515 520 525  
 Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr Met  
 530 535 540  
 Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln  
 545 550 555 560  
 Pro Pro Ala Ala Asn Gln Ser Ile Thr Leu Ser Asn Leu His Leu Ser  
 565 570 575  
 Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn  
 580 585 590  
 Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala  
 595 600 605  
 Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp Asp  
 610 615 620  
 Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asp  
 625 630 635 640  
 Val Leu Lys Leu Gln Leu Gly Thr Gln Pro Pro Ala Asn Ala Pro Ser  
 645 650 655  
 Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly ser  
 660 665 670  
 Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr  
 675 680 685  
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg  
 690 695 700  
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile  
 705 710 715 720  
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr  
 725 730 735  
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp  
 740 745 750  
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
 755 760 765  
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
 770 775 780  
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn  
 785 790 795 800  
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu  
 805 810 815  
 Cys Gly Ser Tyr Val Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
 820 825 830  
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
 835 840 845  
 Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly  
 850 855 860  
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
 865 870 875 880  
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr

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885	890	895
Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn		
900	905	910
Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His		
915	920	925
Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg		
930	935	940
Thr Ile Ser Gly Thr Thr Leu Leu Ser His Gln Glu Thr Trp		
945	950	955
Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly		
965	970	975
Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly		
980	985	990
Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly		
995	1000	1005
Ser Lys Val Arg Phe		
1010		

&lt;210&gt; 16

&lt;211&gt; 1013

&lt;212&gt; PRT

&lt;213&gt; Chlamydia sp.

&lt;400&gt; 16

Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr		
1	5	10
Ser Cys Cys Ser Leu Thr Gly Gly Tyr Ala Ala Glu Ile Met Val		
20	25	30
Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr		
35	40	45
Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu		
50	55	60
Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser		
65	70	75
Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His		
85	90	95
Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu		
100	105	110
Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu		
115	120	125
Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala		
130	135	140
Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser		
145	150	155
Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu		
165	170	175
Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile		
180	185	190
Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe		
195	200	205
Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr		
210	215	220
Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Ile Ala Asn		
225	230	235
Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln		
245	250	255
Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe		
260	265	270
Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly		
275	280	285
Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys		
290	295	300

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Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu  
 305 310 315 320  
 Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp  
 325 330 335  
 Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn  
 340 345 350  
 Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser  
 355 360 365  
 Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys Leu  
 370 375 380  
 Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Gly Asn Ile Ala Asn  
 385 390 395 400  
 Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser  
 405 410 415  
 Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala  
 420 425 430  
 Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala  
 435 440 445  
 Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala  
 450 455 460  
 Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn  
 465 470 475 480  
 Asn Gln Pro Ala Gln Ser Ser Glu Pro Leu Lys Ile Asn Asp Gly Glu  
 485 490 495  
 Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Asn Ser Thr Leu Tyr  
 500 505 510  
 Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala  
 515 520 525  
 Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr Met  
 530 535 540  
 Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln  
 545 550 555 560  
 Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser  
 565 570 575  
 Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn  
 580 585 590  
 Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala  
 595 600 605  
 Gly Pro Val Thr Ile Ser Gly Pro Phe Phe Phe Glu Asp Leu Asp Asp  
 610 615 620  
 Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asp  
 625 630 635 640  
 Val Leu Lys Leu Gln Leu Gly Thr Gln Pro Ser Ala Asn Ala Pro Ser  
 645 650 655  
 Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser  
 660 665 670  
 Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr  
 675 680 685  
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg  
 690 695 700  
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile  
 705 710 715 720

Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr  
 725 730 735  
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Ser Tyr His Asp  
 740 745 750  
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
 755 760 765  
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
 770 775 780  
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn

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## 7969076999.txt

785 790 795 800  
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu  
 805 810 815  
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
 820 825 830  
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
 835 840 845  
 Asp Val Arg Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly  
 850 855 860  
 Leu Pro Ile Val Thr Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
 865 870 875 880  
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr  
 885 890 895  
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn  
 900 905 910  
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His  
 915 920 925  
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg  
 930 935 940  
 Thr Ile Ser Gly Thr Gln Thr Leu Leu Ser His Gln Glu Thr Trp  
 945 950 955 960  
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly  
 965 970 975  
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
 980 985 990  
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
 995 1000 1005  
 Ser Lys Val Arg Phe  
 1010

<210> 17  
 <211> 505  
 <212> PRT  
 <213> Chlamydia sp.

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 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe  
 20 25 30  
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala  
 35 40 45  
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu  
 50 55 60  
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn  
 65 70 75 80  
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu  
 85 90 95  
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val  
 100 105 110  
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr  
 115 120 125  
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu  
 130 135 140  
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp  
 145 150 155 160  
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys  
 165 170 175  
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys  
 180 185 190  
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala  
 195 200 205  
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val

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210	215	220													
Gln	Asp	Gly	Gln	Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro
225					230					235					240
Val	Val	Ser	Phe	Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val
					245				250						255
Ala	Arg	Val	Gly	Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu
			260					265					270		
Asn	Asn	Gly	Lys	Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Ser	Pro	Val	Tyr
			275				280				285				
Ile	Ala	Ala	Lys	Gln	Pro	Thr	Ser	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asn
			290			295				300					
Asn	Tyr	Gly	Asp	Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala
			305		310				315						320
Gly	Ser	Asn	Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val
					325				330						335
Phe	Phe	Ser	Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala
					340			345					350		
Lys	Lys	Leu	Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Arg	Asn
					355		360					365			
Ile	Ala	Asn	Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu
					370		375			380					
Ser	Leu	Ser	Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys
						385				395					400
Arg	Thr	Ala	Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser
						390				405		410			415
Ser	Gln	Ala	Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg
					420			425				430			
Ala	Lys	Ala	Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala
					435		440					445			
Asn	Gly	Asn	Asn	Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu	Leu	Lys	Ile	Asn
					450		455				460				
Asp	Gly	Glu	Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Ser	Ser
						465				470		475			480
Thr	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg
						485			490						495
Glu	Lys	Ala	Lys	Leu	Ser	Val	Asn	Ser							
					500				505						

<210> 18  
<211> 57  
<212> DNA  
<213> Chlamydia sp.

<400> 18 aagggcccaa ttacgcagag ctcgaaqaa attatggattc ctcaaggaaat ttacgat 57

<210> 19  
<211> 20  
<212> DNA  
<213> Chlamydia sp.

<400> 19  
cgctctagaa ctagtggatc 20

<210> 20  
<211> 22  
<212> DNA  
<213> *Chlamydia* sp.

<400> 20  
atgggttcctc aaggaattta cg 22

<210> 21

## 7969076999.txt

<211> 19  
 <212> DNA  
 <213> Chlamydia sp.

<400> 21  
 ggtcccccat cagcgggag

19

<210> 22  
 <211> 1515  
 <212> DNA  
 <213> Chlamydia sp.

&lt;400&gt; 22

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aatttgaca attctattgc agctttgcct	ttaagttgtt	ttggaaactt	180
tttactgttt tagggagagg acactcgtt	actttcgaga	acatacggac	240
ggggcagctc taagtaatag cgctgcgtat	gactgtttt	ctattgaggg	300
ttatccctttt ccaatttgc	ttcattactt	gccgtactgc	360
gttagccaga cttccgacgac	aacatctaca	ccgtctaatg	420
gatctttgt tactcataaa	tgagaagttc	tcattctata	480
gggggagcta tagatgtctaa	gagcttaacg	gttcaaggaa	540
caagaaaata ctgctcaagc	tgatggggga	gcttgcataag	600
atggctaaacg aggctccctat	tgcctttgtt	gcgaatgttg	660
attgtctgtg ttcaggatgg	gcagcaggga	gtgtcatcat	720
gttagtaagt ttcccaagaaa	tactcgttgc	gagtttgatg	780
ggagggattt acttctacgg	gaacgttgc	tccctgaata	840
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ggccctgtac aatttttaag	gaatatcgct	aatgtatggt	1140
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agaacagcca aagagaatgc	tggcgatgtt	aatggctaa	1260
tcgatgggat cggggggaaa	aataacgaca	ttaagagcta	1320
ttaalgtac ccatcgagat	ggcaaacgga	aataaccgc	1380
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ttatcagtga atttct			1515

&lt;210&gt; 23

&lt;211&gt; 3354

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Recombinant Expression Vector

&lt;400&gt; 23

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aacatcacgga cttctacaaa	tggagctgca	ctaagtgcac	gcgctaata	cgggttattt	360
actattgagg gttttaaaga	attatctttt	tccaatttgc	accattact	tgcctactg	420
cctgctgcaa cgactaataaa	ttgttagccag	actccgtcga	caacatctac	accgtctaat	480
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agtaattcag ttctggaga	tggggagct	atagatgcata	agagcttaac	gttcaagga	600
attagcaagc ttgtgttctt	ccaagaaaaat	actgcataag	ctgtatgggg	agcttgcataa	660
gtagtcacca gtttctctgc	tatggcttaac	gaggctctta	ttgcctttgt	agcgaatgtt	720
gcaggagttaa gagggggagg	gattgctgt	gttcaggatg	ggcagcagggg	agtgtcatca	780
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## 7969076999.txt

ggaaacgtag	cccgagtagg	aggagggatt	tactcctacg	ggaacgttgc	tttcctgaat	900
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ccaaacaaatg	gacaaggctc	taatacgagt	gataattacg	gagatggagg	agctatctc	1020
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<210> 24  
 <211> 3324  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

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gagaacatac	gacgttctac	aatgttgcgt	gtcaatgtt	acagcgctaa	tagcgggtta	360
tttactatttgc	agggtttttaa	agaattatctt	ttttcaat	gcaacttattt	acttgcgtt	420
ctgcctgctg	caacgactaa	taatgttgc	cgacttcgtt	cgacaacatc	tacaccgtct	480
aatgttacta	tttattttctaa	aacagatctt	ttgttactca	ataatgttgc	ttgttactt	540
tatagtaattt	tagtctctgg	agatggggga	actatagatgt	ctaagagatctt	aacgggttcaa	600
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&lt;210&gt; 25

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Chlamydia sp.

&lt;400&gt; 25

Pro	Tyr	Thr	Val	Ile	Gly	Asp	Pro	Ser	Gly	Thr	Thr	Val	Phe	Ser	Ala
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Gly	Glu	Leu	Thr	Leu	Lys	Asn	Leu	Asp	Asn	Ser	Ile	Ala	Ala	Pro	Leu
					20			25				30			
Ser	Cys	Phe	Gly	Asn	Leu	Leu	Gly	Ser	Phe	Thr	Val	Leu	Gly	Arg	Gly
					35			40				45			
His	Ser	Leu	Thr	Phe	Glu	Asn	Ile	Arg	Thr	Ser	Thr	Asn	Gly	Ala	Ala
					50			55				60			
Leu															
65															

&lt;210&gt; 26

## 7969076999.txt

<211> 24  
<212> PRT  
<213> Chlamydia sp.

<400> 26  
Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser  
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Ser Leu Leu Ala Asn Asn Ala Val  
20

<210> 27  
<211> 8  
<212> PRT  
<213> Chlamydia sp.

<400> 27  
Gly Tyr Thr Gly Asp Ile Val Phe  
1 5

<210> 28  
<211> 7  
<212> PRT  
<213> Chlamydia sp.

<400> 28  
Tyr Gly Asp Ile Ile Phe Asp  
1 5

<210> 29  
<211> 63  
<212> PRT  
<213> Chlamydia sp.

<400> 29  
Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu  
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Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly  
20 25 30  
Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn  
35 40 45  
Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly  
50 55 60

<210> 30  
<211> 22  
<212> PRT  
<213> Chlamydia sp.

<400> 30  
Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys  
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Ile Asn Asp Gly Glu Gly  
20

<210> 31  
<211> 14  
<212> PRT  
<213> Chlamydia sp.

<400> 31  
Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu  
1 5 10  
<210> 32  
<211> 10  
<212> PRT  
<213> Chlamydia sp.

<400> 32

## 7969076999.txt

Lys Leu Ser Val Asn Ser Leu Ser Gln Thr  
 1 5 10

&lt;210&gt; 33

&lt;211&gt; 45

&lt;212&gt; PRT

&lt;213&gt; Chlamydia sp.

&lt;400&gt; 33

Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile  
 1 5 10 15  
 Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu  
 20 25 30

Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu  
 35 40 45

&lt;210&gt; 34

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Chlamydia sp.

&lt;400&gt; 34

Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile  
 1 5 10 15  
 Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu  
 20 25 30

Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys  
 35 40 45

Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro  
 50 55 60

&lt;210&gt; 35

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Chlamydia sp.

&lt;400&gt; 35

Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr  
 1 5 10

&lt;210&gt; 36

&lt;211&gt; 458

&lt;212&gt; PRT

&lt;213&gt; Chlamydia sp.

&lt;400&gt; 36

Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu  
 1 5 10 15

Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly  
 20 25 30

Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Thr Ser  
 35 40 45

Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe  
 50 55 60

Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn  
 65 70 75 80

Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala  
 85 90 95

Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser  
 100 105 110

Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn  
 115 120 125

Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly  
 130 135 140

Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly  
 145 150 155 160

Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln

7969076999.txt

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Ser	Gly	Glu	Leu	Ser	Leu	Ser	Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp
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Gly	Asn	Leu	Lys	Arg	Thr	Ala	Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly
	210				215						220				
val	Thr	Val	Ser	Ser	Gln	Ala	Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile
					230				235					240	
Thr	Thr	Leu	Arg	Ala	Lys	Ala	Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro
					245				250					255	
Ile	Glu	Met	Ala	Asn	Gly	Asn	Asn	Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu
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Leu	Lys	Ile	Asn	Asp	Gly	Glu	Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala
					275			280			285				
Asn	Gly	Ser	Ser	Thr	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg
	290				295					300					
Ile	Val	Leu	Arg	Glu	Lys	Ala	Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln
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Thr	Gly	Gly	Ser	Leu	Tyr	Met	Glu	Ala	Gly	Ser	Thr	Trp	Asp	Phe	Val
					325				330					335	
Thr	Pro	Gln	Pro	Pro	Gln	Gln	Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr
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Leu	Ser	Asn	Leu	His	Leu	Ser	Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala
					355			360				365			
val	Thr	Asn	Pro	Pro	Thr	Asn	Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala
					370			375			380				
val	Ile	Gly	Ser	Thr	Thr	Ala	Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile
					385			390			395				400
Phe	Phe	Glu	Asp	Leu	Asp	Asp	Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu
					405				410					415	
Gly	Ser	Asn	Gln	Lys	Ile	Asn	Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Lys
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Pro	Pro	Ala	Asn	Ala	Pro	Ser	Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro
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Lys	Tyr	Gly	Tyr	Gln	Gly	Ser	Trp	Lys	Leu						
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<210> 37  
<211> 325  
<212> PRT  
<213> chlamydia sp.

<400> 37  
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg  
 1 5 10 15  
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile  
 20 25 30  
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr  
 35 40 45  
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp  
 50 55 60  
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
 65 70 75 80  
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
 85 90 95  
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn  
 100 105 110  
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu  
 115 120 125  
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
 130 135 140  
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
 145 150 155 160

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Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly  
165 170 175  
Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
180 185 190  
Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr  
195 200 205  
Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn  
210 215 220  
Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His  
225 230 235 240  
Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg  
245 250 255  
Thr Ile Ser Gly Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp  
260 265 270  
Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly  
275 280 285  
Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
290 295 300  
Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
305 310 315 320  
Ser Arg Val Arg Phe  
325

&lt;210&gt; 38

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial sequence: primer

&lt;400&gt; 38

gggtttggga atcagcacat gaaaacctca tatacatttg c

41

&lt;210&gt; 39

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial sequence: primer

&lt;400&gt; 39

gcaaatgtat atgagggtttt catgtgctga ttcccaaacc c

41

&lt;210&gt; 40

&lt;211&gt; 55

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial sequence: primer

&lt;400&gt; 40

aaggggccaa ttacgcagac atatggaaac gtctttccat aagtttttc tttca

55

&lt;210&gt; 41

&lt;211&gt; 80

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial sequence: primer

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<400> 41  
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 ctacttcctg cactcaaacc 80

<210> 42  
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 <212> PRT  
 <213> Chlamydia sp.

<400> 42  
 Glu Ile Met Val Pro Gln 1  
 5

<210> 43  
 <211> 984  
 <212> PRT  
 <213> Chlamydia sp.

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 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe 20 25 30  
 ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala 35 40 45  
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu 50 55 60  
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn 65 70 75 80  
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu 85 90 95  
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val 100 105 110  
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr 115 120 125  
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu 130 135 140  
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp 145 150 155 160  
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys 165 170 175  
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys 180 185 190  
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala 195 200 205  
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val 210 215 220  
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro 225 230 235 240  
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val 245 250 255  
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu 260 265 270  
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr 275 280 285  
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn 290 295 300  
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala 305 310 315 320  
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val 325 330 335  
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala 340 345 350

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Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn  
 355 360 365  
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu  
 370 375 380  
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys  
 385 390 395 400  
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser  
 405 410 415  
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg  
 420 425 430  
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala  
 435 440 445  
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn  
 450 455 460  
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser  
 465 470 475 480  
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg  
 485 490 495  
 Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser  
 500 505 510  
 Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val Thr Pro Gln Pro  
 515 520 525  
 Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu  
 530 535 540  
 His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro  
 545 550 555 560  
 Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser  
 565 570 575  
 Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp  
 580 585 590  
 Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln  
 595 600 605  
 Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn  
 610 615 620  
 Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr  
 625 630 635 640  
 Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly  
 645 650 655  
 Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly  
 660 665 670  
 Pro Glu Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile  
 675 680 685  
 Leu Asp Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly  
 690 695 700  
 Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe  
 705 710 715 720  
 Tyr His Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly  
 725 730 735  
 Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly  
 740 745 750  
 Leu Ala Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys  
 755 760 765  
 Arg Ser Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln  
 770 775 780  
 Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala  
 785 790 795 800  
 Ser Tyr Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala  
 805 810 815  
 Glu Glu Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile  
 820 825 830  
 Gly Ala Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn  
 835 840 845  
 Glu Leu Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu

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850 855 860  
Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His  
865 870 875 880  
Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser  
885 890 895  
Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp  
900 905 910  
Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln  
915 920 925  
Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val  
930 935 940  
Val Arg Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr  
945 950 955 960  
Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu  
965 970 975  
Ser Ala Gly Ser Arg Val Arg Phe  
980